

2/15

1 GTTTTCAAAA TCGGTGGAGG TGCATGAAAA AGTTATTGGG
41 CATTTTTTGA AAATAAAAAA ATATCAATAA GTTGGAGTCA
↓START
81 TTACCGAATT TTTATACTTA TTTGTTTAGA ATGAACTTTA
-35 -10
121 TAACATAGTT GGATAGAGTT TTCGATTTAA TACATTAAAT
161 GTGAACCTTG CTACAACAAG ATGTGCATCA GAAGGAGTGG
RIBOSOME BINDING SITE
201 TTTAATAATG (SEQ ID NO:19)--sarR--TAA (SEQ ID NO:34)

FIG. 1B

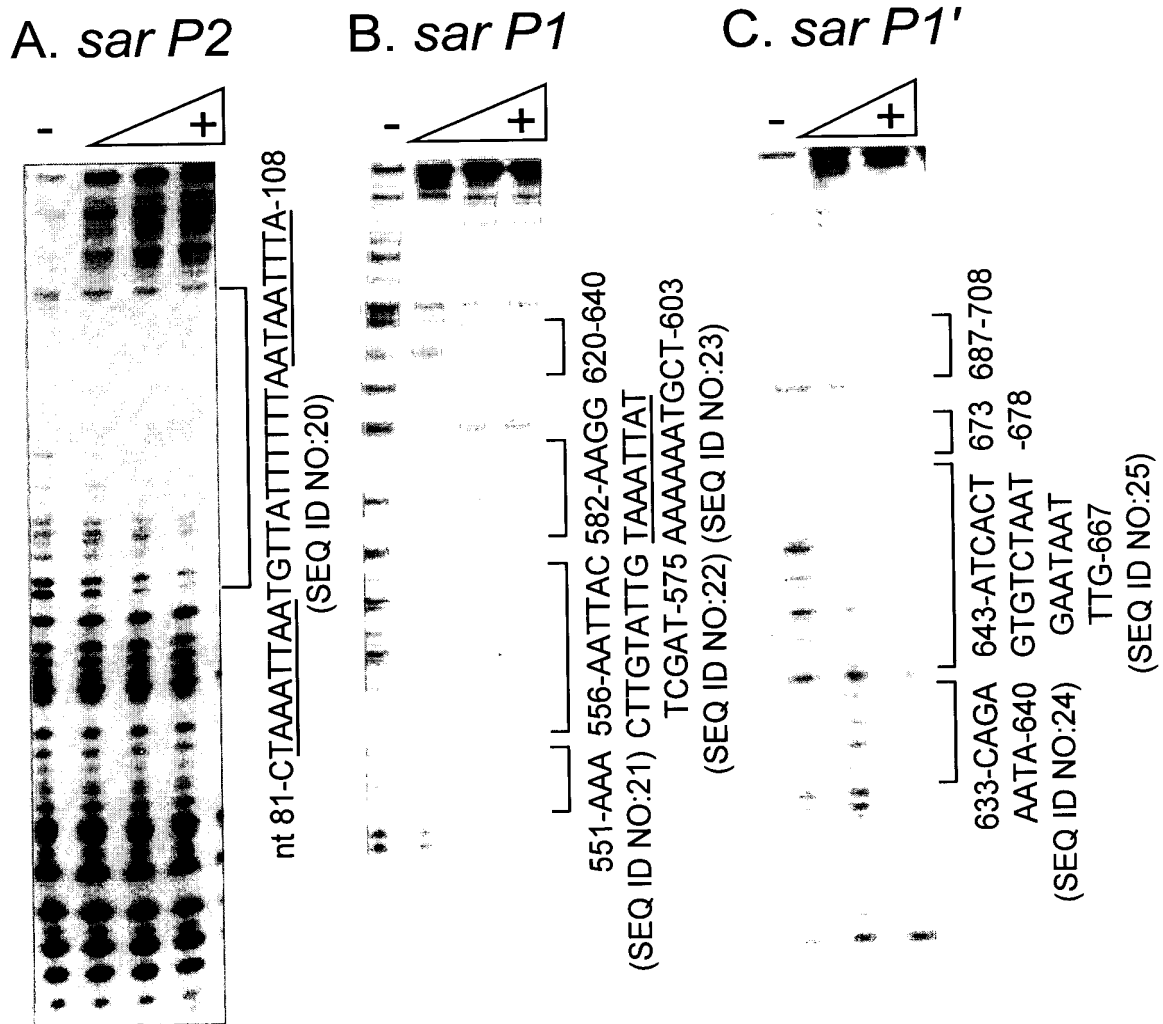
	10	20	30	40
SarR	M--SKINDINDLVNATFQVKKFFRDTKKKFN	LN	YEEI	YILN
	:	:	:
SarA	MAITKINDCFELLSMVTYADKLKSLIKKEFS	IS	FEEF	AVLT
	50	60	70	80
SarR	HILRSESNEISSKEIAKCSEFKPYLTKALQ	KL	KDL	KLLS

SarA	YISENKEKEYYLKDIINHLNYKQPQVVK	AV	KIL	SQEDYFD
	90	100	110	
SarR	QKRILQDERTVIVYVT-----	DTL	KANI	HKLISELEEY
	:	...
SarA	KKRNEHDERTVLILVNAQQRKKIESLL	SR	VN	KRITEANNE
SarR	IKN (SEQ ID NO:2)			
	:.			
SarA	IEL (SEQ ID NO:3)			

FIG. 1C

6/15

FIG. 5



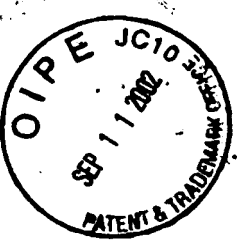
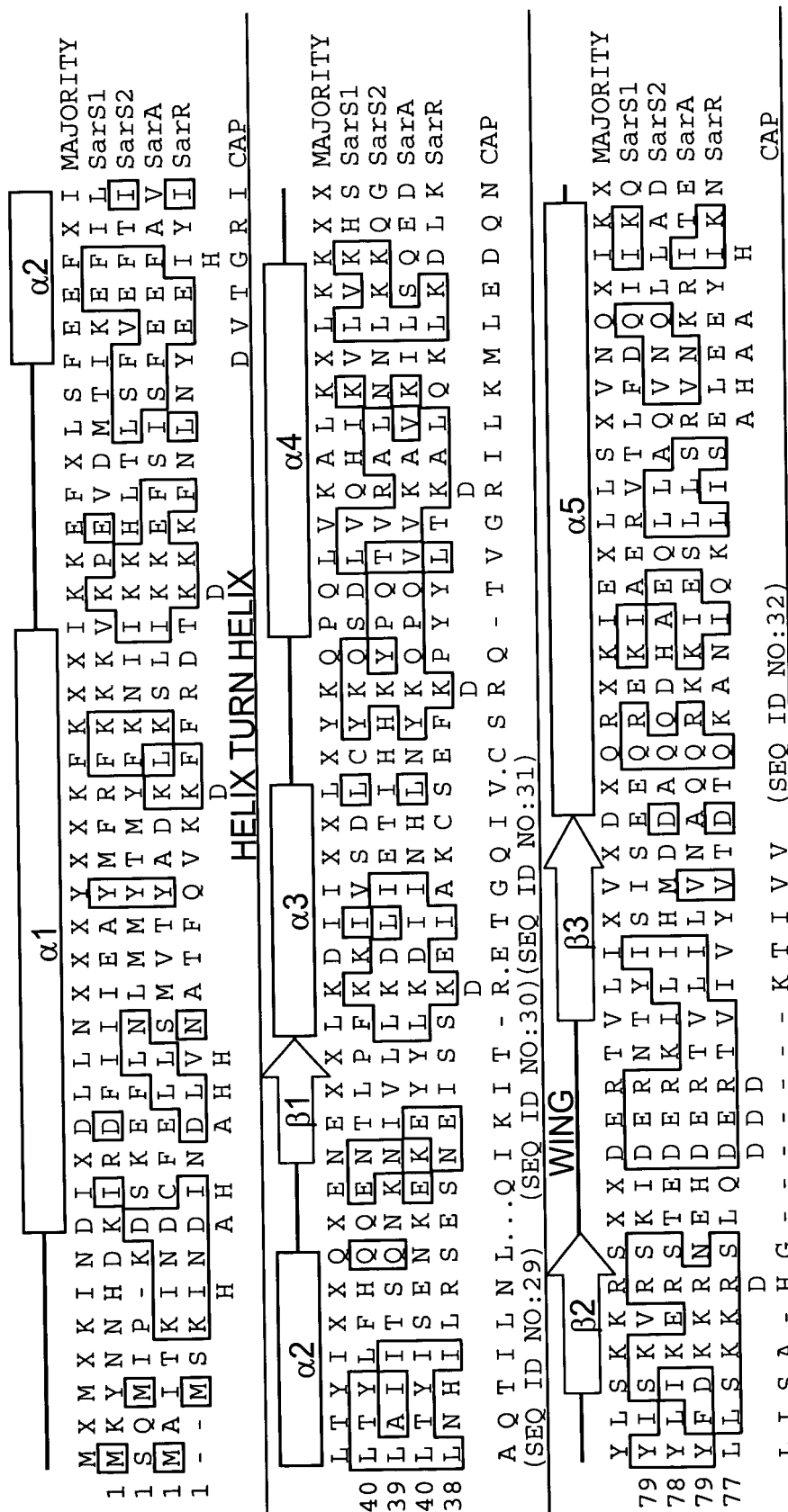


FIG. 11



X N X (SEQ ID NO:26) MAJORITY
119 F N - (SEQ ID NO:27) SarS1
118 - K D (SEQ ID NO:28) SarS2
119 A N (SEQ ID NO:35) SarA
117 - - - (SEQ ID NO:2) SarR